

## SEQUENCE LISTING

<110> Novartis Forschungsstiftung, Zweigniederlassung Friedrich  
Miescher Institute for Biomedical Research

hofsteenge, jan

keusch, jeremy

<120> Assays for C-Mannosyltransferase

<130> 1-32709A

<150> GB0223449.0

<151> 2002-10-09

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic peptide

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Ala Trp Ala Gln Trp Ala  
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<212> DNA

<213> artificial sequence

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<223> synthetic oligonucleotide

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<223> synthetic oligonucleotide

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gctctagaga attcctatca agcccactga gcccaagcgg at  
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48

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1 5 10 15

ctc ctg ggc gtg gca gcc gtg tgc aca atc atc gca ctg tca gtg gtg  
96

Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val  
20 25 30

tac tcc cag gag aag aac aag aac gcc aac agc tcc ccc gtg gcc tcc  
144

Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser  
35 40 45

acc acc ccg tcc gcc tca gcc acc acc aac ccc gcc tcg gcc acc acc  
192

Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr  
 50 55 60

ttg gac caa agt gag aat ttg tat ttt cag ggt act agt tcc cct ata  
 240

Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile  
 65 70 75 80

cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc act cga ctt ctt  
 288

Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu  
 85 90 95

ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg tat gag cgc gat  
 336

Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp  
 100 105 110

gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg ggt ttg gag ttt  
 384

Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe  
 115 120 125

ccc aat ctt cct tat tat att gat ggt gat gtt aaa tta aca cag tct  
 432

Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser  
 130 135 140

atg gcc atc ata cgt tat ata gct gac aag cac aac atg ttg ggt ggt  
 480

Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly  
 145 150 155 160

tgt cca aaa gag cgt gca gag att tca atg ctt gaa gga gcg gtt ttg  
 528

Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu  
 165 170 175

gat att aga tac ggt gtt tcg aga att gca tat agt aaa gac ttt gaa  
 576

Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu  
 180 185 190

act ctc aaa gtt gat ttt ctt agc aag cta cct gaa atg ctg aaa atg  
624

Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met  
195 200 205

ttc gaa gat cgt tta tgt cat aaa aca tat tta aat ggt gat cat gta  
672

Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val  
210 215 220

acc cat cct gac ttc atg ttg tat gac gct ctt gat gtt gtt tta tac  
720

Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr  
225 230 235 240

atg gac cca atg tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa  
768

Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys  
245 250 255

aaa cgt att gaa gct atc cca caa att gat aag tac ttg aaa tcc agc  
816

Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser  
260 265 270

aag tat ata gca tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt  
864

Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly  
275 280 285

ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt gga tcc gct tgg  
912

Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ala Trp  
290 295 300

gct cag tgg gct  
924

Ala Gln Trp Ala  
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<211> 308

<212> PRT

<213> artificial sequence

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<400> 9

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20 25 30

Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser  
35 40 45

Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr  
50 55 60

Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile  
65 70 75 80

Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu  
85 90 95

Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp  
100 105 110



Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe  
115 120 125

Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser  
130 135 140

Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly  
145 150 155 160

Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu  
165 170 175

Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu  
180 185 190

Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met  
195 200 205

Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val  
210 215 220

Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr  
225 230 235 240

Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys  
245 250 255

Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser  
260 265 270

Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly  
275 280 285

Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ala Trp  
290 295 300

Ala Gln Trp Ala  
305